

RESULT 1
 US-10-665-883A-4
 ; Sequence 4, Application US/10665883A
 ; GENERAL INFORMATION:
 ; APPLICANT: YUAN, Chong-Sheng
 ; TITLE OF INVENTION: DETERMINATION OF IONS USING ION-SENSITIVE ENZYMES
 ; FILE REFERENCE: 466992001100
 ; CURRENT APPLICATION NUMBER: US/10/665,883A
 ; CURRENT FILING DATE: 2003-09-19
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 392
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimeric protein
 US-10-665-883A-4

Query Match 100.0%; Score 2047; DB 36; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.4e-192;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1
 Qy 1 MGSGDDDDLALALERELLVATQAVRKASLLTKRIQSEVISHKDDSTTITKNDNSPVTIGD 60
 Db 1 MGSGDDDDLALALERELLVATQAVRKASLLTKRIQSEVISHKDDSTTITKNDNSPVTIGD 60
 Qy 61 YAAQTIINAIAKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFT 120
 Db 61 YAAQTIINAIAKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFT 120
 Qy 121 NDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTGKFLRGEQFAVCLALIVDGVVQ 180
 Db 121 NDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTGKFLRGEQFAVCLALIVDGVVQ 180
 SEQ 2
 Qy 181 LGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHRHLKDTK 240
 Db 181 LGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHRHLKDTK 240
 Qy 241 DMITLEGVEKGHSSHDEQTAIKNKLNIKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQ 300
 Db 241 DMITLEGVEKGHSSHDEQTAIKNKLNIKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQ 300
 Qy 301 EKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNRGTILATKGVIASSGPRELHDLVSVTSC 360
 Db 301 EKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNRGTILATKGVIASSGPRELHDLVSVTSC 360
 SEQ 3
 Qy 361 DVIQSRNAKGELEGLPIPNPLRLTGHSHHHHHH 392
 Db 361 DVIQSRNAKGELEGLPIPNPLRLTGHSHHHHHH 392

note that current SEQ 4 has only 6 his, not 7.

NOTE it appears that SEQ ID NO:2 was previously known 100%; however the combination of SEQ 2, 3 and 1 may be their true invention, if I can not find reason to do....???

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RESULT 1
S35318
MET22 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: HAL2 protein; protein O1180; protein YOL064c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S35318; S66757
R;Glaeser, H.U.; Thomas, D.; Gaxiola, R.; Montrichard, F.; Surdin-Kerjan, Y.;
Serrano, R.
EMBO J. 12, 3105-3110, 1993
A;Title: Salt tolerance and methionine biosynthesis in Saccharomyces
cerevisiae involve a putative phosphatase gene.
A;Reference number: S35318; MUID:93345455; PMID:8393782
A;Accession: S35318
A;Molecule type: DNA
A;Residues: 1-357
A;Cross-references: UNIPROT:P32179; UNIPARC:UPI00001120E7; EMBL:X72847;
NID:g298022; PIDN:CAA51361.1; PID:g298023
R;Alexandraki, D.; Katsoulou, C.; Tzermia, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66756
A;Accession: S66757
A;Molecule type: DNA
A;Residues: 1-357
A;Cross-references: UNIPARC:UPI00001120E7; EMBL:Z74806; NID:g1419882;
PID:g1419883; MIPS:YOL064c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MET22; HAL2
A;Cross-references: SGD:S0005425; MIPS:YOL064c
A;Map position: 15L
C;Keywords: transmembrane protein
F;157-173/Domain: transmembrane #status predicted

Query Match          100.0%;   Score 1838;   DB 2;   Length 357;
Best Local Similarity 100.0%;   Pred. No. 4.1e-140;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

Qy          1  ALERELLVATQAVRKASLLTKRIQSEVISHKDDSTTITKNDNSPVTGTGYAAQTTIINAIAK 60
           |||||||
Db          2  ALERELLVATQAVRKASLLTKRIQSEVISHKDDSTTITKNDNSPVTGTGYAAQTTIINAIAK 61

Qy          61  SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV 120
           |||||||
Db          62  SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV 121

Qy          121 RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS 180
           |||||||
Db          122 RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS 181

Qy          181 SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH 240
           |||||||
Db          182 SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH 241

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Qy      241 SSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVLRRLPIKLSYQEKIWDHAAGNVI 300
        |||
Db      242 SSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVLRRLPIKLSYQEKIWDHAAGNVI 301

Qy      301 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 356
        |||
Db      302 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 357

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Interesting post filing application by same inventor:

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RESULT 1
US-11-881-179-1
; Sequence 1, Application US/11881179
; Publication No. US20080096230A1
; GENERAL INFORMATION
; APPLICANT: YUAN, Chong-Sheng
; APPLICANT:DATTA, Abhijit
; APPLICANT:LIU, Limin
; TITLE OF INVENTION: METHODS FOR ASSAYING PERCENTAGE OF GLYCATED HEMOGLOBIN
; FILE REFERENCE: 466992002000
; CURRENT APPLICATION NUMBER: US/11/881,179
; CURRENT FILING DATE: 2007-11-21
; PRIOR APPLICATION NUMBER: US 60/833,390
; PRIOR FILING DATE: 2006-07-25
; PRIOR APPLICATION NUMBER: US 60/858,809
; PRIOR FILING DATE: 2006-11-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fructosyl amino acid oxidase
US-11-881-179-1

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Query Match          9.9%; Score 203.5; DB 2; Length 472;
Best Local Similarity 23.0%; Pred. No. 5.3e-13;
Matches 122; Conservative 50; Mismatches 161; Indels 197; Gaps
25;

Qy      1 MGGSGDDDDLLALALERE---LLVATQAVRKASLLTKRIQSEVISHKDDSTITKNDNSPVT 57
        |||: : | : : : | : |
Db      1 MGGSGDDDDLLALAVTKSSSLLIVGAGTGTSTALH-----LARRGYTNVTVLDPPYVPV 53

Qy      58 TGDYAAQTIIINAISNFPDDKVVGEESSSGLSDAFVSGILNEIKA-----NDEVYN 109
        :|| : :||: | | :|| | || :
Db      54 -----SAISAGNDVNKVISSGQYSNNKDEIE---VNEILAEAFNGWKNDPLFK 99

Qy      110 KNYKKDDFLFT-----NDQFPLKSLEDVRQIIDFGNYE 142
        | | : :|| : | | | || :

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Db      100  PYYHDITGLLSACSQEGDLRLGVVRVPGEDPNLVELTRPEQFRKLAPEGVQLQ-GDFPGWK 158
Qy      143  G--GRKGRFWCLDPIDGTGKFLRGEQFAVCLAL-IVDGVVQLGCGICPNLVSSYGAQDL 199
      | | | | : : | : | | : | : |
Db      159  GYFARSGAGWA---HARNALVAAAREAQRMGVKFVTGTPQ-----GRVVTLIFENNDV 208
Qy      200  KGH-ESFGYIFRAVR-----GLGAF--YSPSSDAESWTKIHVRHLKDT----KDMIT 244
      || | | | | : | : | : | : | : |
Db      209  KGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA-LKPEERALYKNIPV 267
Qy      245  LEGVEKG--HSSHDEQTAIK-----NKLNISKSLH----- 272
      : : | : : | : | : | : | : | : |
Db      268  IFNIERGFFFEPEERGEIKICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRL 327
Qy      273  -----LDSQAKYCLLALGLADV---YLRLEPIKLSY 299
      : | : | | | : | : |
Db      328  LKETMPQLADRPFSSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLP---- 382
Qy      300  QEKIWDHAAGNVIVHEAGGIHTDAME-----DVPLDFGNGRLLATKGVIA 344
      : | : | : | | | : | : | : | : |
Db      383  -----SIGNLIV-----DAMEGKVPQKIHelikWNPDIANRNWRDILGRFG--- 424
Qy      345  SSGPR---ELHDLVSTSCDVIQSRNAKGELEGLPIPNPLLRTGHHHHHH 391
      || | : | : | : | | | | | | | | | |
Db      425  --GPNRVMDFHDVKEWTNVOYRDISKLGKELEGLPIPNPLLRTGHHHHHH 472

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